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FIGURE 458

MQAKYSSTRDMLDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCVLVLI
GLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRELY
NKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAASQSY
SEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSPPSRDCVAILNGMIFSKDCKEL
KRCVCERRAGMVKPESLHVPPETLGED

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FIGURE 459

GT TGATGGCAAAC TCTCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCAC
TGGCGGCCCGCAACACTCCGTCTCACCTCTGGGCCCACTGCATCTAGAGGAGGGCCGTCTGT
GAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTGAGAAGCTGGCCAGGGTGGTGGT
CAGCTGGGTGAGGACCTACGGACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAGGGAA
GTGGGAGCCTCGAGCCCTCGGGTGAAGCTGACCCCAAGCCACCTTACCTGGACAGGATGA
GAGTGTGAGGTGTGCTTCGCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGATGTTTA
TTCGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCAGCCTCGC
CCACCAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCCAGCCAACT
ACTTTGCGTTTAAATCTGCAGTGGGGCCGCCAACGTCGTGGGCCCTACTATGTGCTTTGAAG
ACCGCATGATCATGAGTCTGTGAAAAACAATGTGGGCAGAGGCCTAAACATCGCCCTGGTGA
ATGGAACCACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGGAGATGTTATGC
ACCTAGTGAAATTCCTTAAAGAAATTCGGGGGGTGCCTGAGTGGTGGTGGTGGCTCCTACGACG
ATCCAGGGACCAAAATGAACGATGAAAGCAGGAAACTCTTCTGACTTGGGGAGTTCTTACG
CAAAACAAC TGGGCTTCGGGACAGCTGGGTCTTCATAGGAGCCAAAGACCTCAGGGGTAAAA
GCCCCTTTGAGCAGTTCTTAAAGAACAGCCAGACACAAACAAATACAGGGGATGGCCAGAGC
TGCTGGAGATGGAGGGCTGCATGCCCCGAAGCCATTTTAGGGTGGCTGTGGCTCTTCTCAG
CCAGGGGCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCGGCAGGGGCTGAGGAGGA
GGAGCAGGGGGTGTGCGTGGAAGGTGCTGCAGGTCCTTGCACGCTGTGTCGCGCTCTCCTC
CTCGGAAACAGAACCCTCCACAGCACATCTACCCGGAAGACCAGCCTCAGAGGGTCCTTCT
GGAACCAGCTGTCTGTGGAGAGAATGGGGTGTCTTCGTGAGGGACTGCTGACGGCTGGTCTGT
AGGAAGGACAACTGCCAGACTTGAGCCCAATTAAATTTTATTTTGTGCTTTTGAAAAAA
AAAAAAAAAAAAA

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FIGURE 460

MRVSGVLRLLALIFAIVTTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCPA
NYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSGDV
MHLVKFLKEIPGGALVLVASYDDPGTKMNDESRLKFSDLGSSYAKQLGFRDSWVFIGAKDLRG
KSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF

Important features:**Signal peptide:**

amino acids 1-15

ATP/GTP-binding site motif A (P-loop).

amino acids 184-191

N-glycosylation site.

amino acids 107-110

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FIGURE 461

AAACTCAGCACTTGCCGGAGTGGCTCATTGTTAAGACAAAGGGTGTGCACCTCCTGGCCAGGA
AACCTGAGCGGTGAGACTCCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACTTCCTC
TAGAACCCGACCCACCACCATGAGGTCCTGCCTGTGGAGATGCAGGCACCTGAGCCAAGCGGT
CCAGTGGTCTTGCTTCTGGCTGTCTGGTCTTCTTTCTTCCGCTTGCCCTCTTTTATTAA
GGAGCCTCAAACAAAGCCTTCCAGGCATCAACGCACAGAGAATTAAGAAAGGTCTCTACA
GTCCCTGGCAAGGCTTAAGTCCCAGGCACCCACAAGGGCGAGGAGGACAACCATCTATGCAGA
GCCAGCGCCAGAGAACAAATGCCCTCAACACACAAAACCCAGGCCAAGGCCACACACCGGAGA
CAGAGGAAAGGAGGCCAACACGGCACCGCCGGAGGAGCAGGACAAGGTGCCCCACACAGCACA
GAGGGCAGCATGGAAGAGCCCAGAAAAAGAGAAAACCATGGTGAACACACTGTCACCCAGAGG
GCAAGATGCAGGGATGGCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCCAGGACACAAA
GACGACCCAGGAATGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGACGGTGTCTAGAGAA
GCACAGGGCAAAGCGGCCAACACAGCCAAGACGCTCATTCCCAAAAGTCAGCACAGAATGCT
GGCTCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCCAGCAGTCTATCCC
ACCTAAGGAGAAGAAACCTCAGGCCACCCCAACCCCTGCCCCCTTCCAGAGCCCCACGACGCA
GAGAAACCAAGACTGAAGGCCGCCAACTTCAAATCTGAGCCTCGTGGGATTTTGAGGAAAA
ATACAGCTTCGAAATAGAGGCTTTCAGACGACTTGCCCTGACTCTGTGAAGATCAAGGCTC
CAAGTCGCTGTGGCTCCAGAAACTCTTCTGCCCAACCTCACTCTCTTCTGGACTCCAGACA
CTTCAACCAGAGTGAGTGGGACCGCTGGAACACTTTGCACCACCTTTGGCTTCATGGAGCT
CAACTACTCCTTGGTGAGAAAGGTCTGTACACGCTTCCCTCCAGTGCCCCAGCAGCAGCTGCT
CCTGGCCAGCTCCCCGCTGGGAGCCTCCGGTGCATCACTGTGCCGTGGTGGGCAACGGGGG
CATCTGAACAACTCCACATGGGCCAGGAGATAGACAGTCAGACTACGTGTTCCGATTGAG
CGGAGCTCTCATTAAGGCTACGAACAGGATGTGGGGAAGTGGGACATCCTTCTACGGCTTAC
CGCCTTCTCCTGACCCAGTCACTCCTTATATTGGGCAATCGGGGTTTCAAGAACGTGCCTCT
TGGGAAGGACGTCCGCTACTTGCACCTTCTGGAAGGCACCCGGGACTATGAGTGGCTGGAAGC
ACTGCTTATGAATCAGACGGGTGATGTCAAAAAACCTTTCTGGTTCCAGGCACAGACCCAGGA
AGCTTTTCGGGAAGCCCTGCACATGGACAGGTACCTGTGTCTGCACCCAGACTTTCTCCGATA
CATGAAGAACAGGTTTCTGAGGTCTAAGACCCTGGATGGTGGCCACTGGAGGATATACCGCCC
CACCCTGGGGCCCTCTGTCTGCTCACTGCCCTTCAGCTCTGTGACCAGGTGAGTGCTTATGG
CTTCACTCACTGAGGGCCATGAGCGCTTTCTGTACTACTATGATACATCATGGAAGCGGCT
GATCTTTTACATAAACCATGACTTCAAGCTGGAGAGAGAAGTCTGGAAAGCGGCTACACGATGA
AGGGATAATCCGGCTGTACCAAGCGTCTGGTCCCGGAAGTGCCTAAAGGCCAAGAACTGAACCGGG
GCCAGGGCTGCCATGGTCTCCTTGCTGCTCCAAGGCACAGGATACAGTGGAATCTTGAGAC
TCTTTGGCCATTTCCCATGGCTCAGACTAAGCTCCAAGCCCTCAGAGTTCCAAGGGAACAC
TTGAACCATGGACAAGACTCTCAAGATGGCAAAATGGTAATTGAGGTTCTGAAGTTCTTCA
GTACATTGCTGTAGGTCTGTAGGCCAGGGATTTTAAATTAATGGGGTGATGGGTGGCCAATA
CCACAATTCCTGCTGAAAAACACTCTCCAGTCCAAAAGCTTCTTGATACAGAAAAAAGAGCC
TGGATTACAGAAACATATAGATCTGGTTGAATTCAGATCGAGTTTACAGTTGTGAATCT
TGAAGGTATTAATTAACTTCACTACAGATGTCTAGAAGACCTTTCTAGGAGTTATCTGATTC
TAGAAGGCTTATACTTGCTTGTCTTAACTTTGACAACCTTACGTGCTCTGTAGAAAAAC
TGATAATAATACAAATGATTGTTGTCCATGGAAAGGCCAAATAAATTTTCTACAGTGAAAAAA
AAAAAAA

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FIGURE 462

MRSCLWRCRHLSQGVQWSLLLVFLFALPSFIKEPQTKPSRHQRTENIKERSLQSLAKPK
SQAPTRARRTTIYAEPAPENNALNTQTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAWKS
PEKEKTMVNTLSPRGQDAGMASGRTEAQSWSQDTKTTQGNQGQTRKLTASRTVSEKHQGKAA
TTAKTLIPKSQHRLAPTGA VSTRTRQKGVTAVIPPEKEKKQATPPPAPFQSPTTQRNQRK
AANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFLPNLTLFLDSRHFNQSEW
DRLEHFAPPFQGMELNYSLVQKVVTFRPPVPQQQLLLASLPAGSLRCITCAVVGNGGILNNSH
MGQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGFATAFSLTQSLILGNRGFKNVPLGKD VRY
LHFLEGTRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFFREALHMDRYLLHPDFLR YMKNRFL
RSKTLTDGAHWRIYRPTTGALLLLTALQLCDQVSAYGFITEGHERFSDHYDYTSWKRLIFYINH
DFKLEREVWKRHLHDEGIIRLYQRPGPGTAKAKN

Important features:**Cytoplasmic Domain:**

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Lumenal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

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FIGURE 463

GGGGGAGCTAGGCCGGCGGCAGTGGTGGTGGCGGCGGCCAAGGGTGAGGGCGGCCCCAGAAC
CCCAGGTAGGTAGAGCAAGAAATGTTGTTTCTGCCCCCTCAAATGGTCCCTTGCAACCATGTCT
ATTTCTACTTTCCCTCACTGTTGGCTCTCCTTAACGTGTGCCACTCCTTCATGGTGTCTAGAGCAC
TGAAGCATCTCCAAAACGTAGTGATGGGACACCATTTCCCTTGAATAAAATACGACTTCTCTGA
GTACGTCATCCCACTTCATTATGATCTCTTGATCCATGCAAACTTACCACGCTTACCTGACCTCTG
GGGAACCAAGAAATAGAAATCACAGCCAGTCAGCCACCAGACCATTATCCTGCTAGATGCA
CCACTGCGAGATATCTAGGGCCACCTCAGGAAGGGAGCTGGAGAGAGGCTATCGGAAGAACCC
CCTGCAAGTCTTGAACACCCCCCTCAGGAGCAATTCGACTGCTGGCTCCCGAGGCCCTCTCT
TGTGCGGCTCCCGTACACAGTTGTCTATTCTACTATGCTGGCAATTTCTGGAGACTTTCCACGG
ATTTTACAAAGCACCTACAGAACCAAGGAAGGGGAACGTAGGATACATAGACTCACACAAAT
TGAACCCACTGCACTAGAAATGGCCTTTCCCTGCTTTGATGAACCTGCTCTCAAAGCAAGTTT
CTCAATCAAATTAGAAGAGAGGCCAAGGCACCTAGCCATCTCCAATATGCCATTGGTGAATC
TGTGACTGTTGCTGAAGGACTCATAGAAGACCAATTTGATGTCACTGTGAAGATGAGCACCTA
TCTGGTGGCCTCATCATTTTCAGATTTTGAGTCTGTGACAGAATAACCAAGAGTGGAGTCAA
GGTTTCTGTTTATGCTGTGCCAGACAAGATAAAATCAAGCAGATTATGCATGGATGCTGCGGT
GACTCTTCTAGAATTTTATGAGGATTATTTTCAGCATACCGTATCCCCTACCCAAACAAGATCT
TGCTGCTATTTCCCGACTTCAGTCTGGTGTATGGAATACTGGGACGTGACAAACATATAGAGA
ATCTGCTCTGTTGTTTGAATGCAAGAAAGTCTTCTGCATCAAGTAAAGTCTGGCATCACAGTGAC
TGTGGCCATGAACGTGGCCACACAGTGGTTTGGGAACCTGGTCACTATGGAATGGTGGGAATGA
TCTTTGGCTAAATGAAGGATTTCGCAAAATTTATGGAGTTTGTGCTCTGCACTGTGACCATCTC
TGAACGTGAAGTGTGGAGATTATTTCTTTGGCAATGTTTGAAGCAATGGAGGTAGATGCTTT
AAATCTCTCACACCTGTGTCTACACCTGTGGAATACTCTGCTCAGATCCGGGAGATGTTTGA
TGATGTTTCTTATGATAAGGGAGCTTGTATTTCTGAATATGCTAAGGGAGTATCTTAGCGCTGA
CGATTTTCAAAGTGGTATTTGTACAGTATCTCCAGAAGCATAGCTATAAAATACAAAACCA
GGACCTGTGGGATAGTATGGCAAGTATTTGCCCTACAGATGGTGTAAAGGGATGGATGGCTT
TTGCTTGAAGATCAACTCTTCACTCTCACATTGGCATCAGGAAGGGTGGATGTGA
AACCATGATGAACACTTGGCACTGCAAGGGGTTTCCCTTAATAACCATCACAGTGAAGGG
GAGGAATGTACACATGAAGCAAGAGCACTACATGAAGGGCTCTGACGGCGCCCCGACACTGG
GTACCTGTGGCATGTTCCATTGACATTATCACACCAAGCAATCAACATGGTCCATCGATTTTT
GCTAAAAACAAAACAGATGTGCTCATCTCCAGAAAGAGGTGGAATGGATCAAAATTTAATGT
GGGCATGAATGGCTATTACATTGTGCATTACGAGGATGATGGATGGGACTCTTTGACTGGCCT
TTTAAAGAGGACACACACAGCAGTCAAGCAGTATGATCGGGCAAGTCTCATTAACAATGCAAT
TCAGCTCGTCAGCATTTGGGAAGCTGTCCATTGAAAAGGCTTGGATTTATCCCTGTACTTGAA
ACATGAACTGAAATTTATGCCCGTGTTCAGAGTTTGAATGAGCTGATTCCTATGTATAAGTT
AATGGAGAAAAGAGATATGAATGAAGTGGAACTCAATTCAAGGCCCTTCCCTATCAGGCTGCT
AAGGGACCTCATTTGATAGCAGACATGGACAGACGAGGGCTCAGTCTCAGAGCAATGCTGCG
GAGTGAACCTACTACTCTCGCTGTGTGCACAACTATCAGCCGTGCTGACAGAGGGCACAAGG
CTATTTTCAGAAAGTGAAGGAATCCAATGGAACCTTGAGCCTGCCTGTGACGCTGACCTTTGGC
AGTGTGTTGCTGTGGGGGCCAGAGCACAGAAGGCTGGGATTTCTTTATAGTAAATATCAGTT
TTCTTTGTCCAGTACTGAGAAAAGCCAAATTTGAATTTGCCCTCTGCAAGAACCCAAATTAAGGA
AAAGCTTCAATGGCTACTAGATGAAAGCTTTAAGGGAGATAAAATAAAAACCTCAGGAGTTTCC
ACAAATTTCTTACATCATTTGGCAGGAACCCAGTAGGATACCCATGCCCCTGGCAATTTCTGAG
GAAAACCTGGAACAACTTGTACAAAAGTTTGAATTTGCTCATCTTCCATAGCCCACTGGT
AATGGGTACAAACAAATCAATTTCTCCAAAGAACACGGCTTGAAGAGAGTAAAGAGGATTTCTCAG
CTCTTTGAAGAAGAAATGGTTCCTCAGCTCCGTTGTGTCACAGACATTAAGAACATTAAGA
AAACATCGGTTGGATGGATAAGAATTTTGATAAAATCAGAGTCTGGCTGCAAGTGAAAGCT
TGAAGCTATGTAATAATTCCTCCCTTGCCCGGTTCCCTGTTATCTCTAATCACCAACATTTTGT
TGAGTGTATTTTCAAACCTCAGAGATGGCTGTTTGGCTCCAAGTGGAGATCTTTTTTCCCTTC
AACTCATTTTGTACTATCCCTGTGAAAAGAAATAGCTGTAGTTTTTCATGAATGGGCTTTTT
CATGAATGGCTATGCTATACCATTGTGTTTTGTTTATCAGAGTGTGGCTTGCAACCTAAACC
CAAGTGTGGGTTTCCCTGCCACAGAGAATAAAGTACCTATTCTTCTCAAAAAAAAAAAAAA
AAAAAAAAAAAAA

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FIGURE 464

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTFPWNKIRLPEYVIPVHY
DLLIHANLTTLTFTWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPQLVLEHP
PQEQIALLAPEPLLVLGPLYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTAARM
AFPCFDEPAFKASFISIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLVAFIIS
DFESVSKITKSGVKVSVYAVPDKINQADYALDAAVTLLEFYEDYFSIPYPLPKQDLAAIPDFQ
SGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHELAHQWFGNLVTMEWWNDLWLNNEG
AKFMEFVSVSVTHPELKVGDYFFGKCFDAMEVDALNSSHEVSTPVENPAQIREMFDDVSYDKG
ACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKMGDMGFCRSQS
SSSSHHWQEGVDVKMTMMNTWTLQRGFPLITITVGRNVHMKQEHYMKGSDGAPDTGYLWHVPL
TFITSKSNMVHRFLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSLTGLLKGTHTA
VSSNDRASLINNAFQLVVSIGKLSIEKALDLSLYLKHETEIMPVFQGLNELIPMYKLMEKRDMN
EVETQFKAFLIRLLRDLDKQTTWDEGSVSEQMLRSELLLLACVHNYPQCVQRAEGYFRKWKE
SNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSTEKSQIEFALCRTQNKEKLQWLDD
ESFKGDKIKTQEFQILTILGRNPVGYPLAWQFLRKNWNKLQVKFELGSSSIAHVMVGTNTQF
STRTRLEEVKGFFSSLKENGSQLRCVQQTITETIEENIGWMDKNFDKIRVWLQSEKLERM

Important features:**Signal peptide:**

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metallopeptidases, zinc-binding region signature:

amino acids 350-360

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FIGURE 465

CAGCCACAGACGGGTC**ATG**AGCGCGGTATTACTGCTGGCCCTCCTGGGGTTTCATCCTCCCACT
GCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTTCAGCATGTGTGGAAGGTGTCCGA
CCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCAGGACAC
GTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGGAGGC
CAAGGACAGGAGCCCCGCGCTCACTGAGCACCGGATGGGCCCGGCTCTCCCTGATCTCCTA
CACCTTCGTGTGCCGCCAGGAGACTTCTGCAACAACTCGTTAACTCCCTCCCGCTTTGGGC
CCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGGAAGGCTG
TCTGGAGGGGACAACAGAAGAGATCTGCCCAAGGGGACCACACACTGTTATGATGGCCTCCT
CAGGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCCCCAGCCAGG
TTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGAACTGCAATAG
GAAAGATTTTCTGACCTGTCTCGGGGGACCACCATTATGACACACGGAAACTTGGCTCAAGA
ACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGTGTGTCAGGAGAC
GCTGTGCTCATAGATGTAGGACTCACATCAACCTGGTGGGGACAAAAGGCTGCAGCACTGT
TGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCCTCTGGGGTGCTTGTGGCCTC
CTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAGCAGCGTTCTGCTGAA
CTCCCTCCCTCCTCAAGCTGCCCTGTCCCAGGAGACCGGCAGTGTCTACCTGTGTGCAGCC
CCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGGGGCGCCACTCATTGTTA
TGATGGGTACATTTCATCTCTCAGGAGGTGGGCTGTCCACCAAAATGAGCATTACAGGGCTGCGT
GGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGA
GAAGCGTGATGTGCAGCCTCTGCTCTCAGCATGAGGGAGGTGGGGCTGAGGGCCTGGAGTC
TCTCACTTGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTGGTGGGGAGTGGTTTGCCCTTC
CTGCT**TAA**CTCTATTACCCCCACGATTCTTACCAGCTGCTGACCAACCACACTCAACCTCCCTC
TGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTCCATTCTGTCCATGAATCATCTT
CCCCACACAAATCATTCATATCTACTCACCTAACAGCAACACTGGGGAGAGCCTGGAGCATC
CGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTGGCTGCATGTATCTGATAATACAGAC
CCTGTCCTTTCA

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FIGURE 466

MSAVLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDITLMLIE
SGPQVSLVLSKGCTEAKDQEPRVTEHRMGPLSLISYTFVCRQEDFCNNLVNSLPLWAPQPPA
DPGSLRCPVCLSMEGCLEGTTEEICPKGTTTCYDGLLRRLRGGGIFSNLRVQGCMPPQPGCNLLN
GTQEIGFVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTSTNTMCEVGVQCQETLLIID
VGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLNCSSSSSVLLNSLPFQ
AAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLGGGLSTKMSIQGCVAQPSS
FLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESITWGVGLALAPALWWGVVCPSC

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FIGURE 467

GAGGATTGGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGAGCCCTTGAGACATCCTTG
AGAAGAGCCACAGCATAAGAGACTGCCCTGCTTGGTGTTTTGCGAGGATGATGATGGTGGCCCTTCG
AGGAGCTTCTGCAATTGCTGGTTCTGTTCCTTGCAGCTTTCTGCCCCCGCCGCACTGTGATCCCA
GGACCCAGCCATGCTGTCATTACATCTACCAGCGCTTTCGAGTCTTGGAGCAAGGGCTGGAAAA
ATGTACCCCAAGCAACGAGGGCATACATTCAGAATTCGAAGAGTTC'CAAAAAATATATCTGT
CATGCTGGGAAGATGTGAGACCTACACAAGTGAGTACAAAGATGTCAGTGGGTAACCTTGGCACT
GAGAGTTGAACGTGCCAACGGGAGATTGACTACATACAATACCTTCGAGAGGGCTGACGAGTG
CATCGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAAGAGAAAA
GATCCGGACTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGCTTTTGAANAAT
AGTGAAGAAGATGATGGACACACATGGCTCTTGGATGAAGAATGCTGCTATAAATCTCCAAA
GGTGTACTTTATTAATTGGATCCAGAAACAACACTGTTTGGGAATTTGCAACACATACGGGCATT
CATGGAGGATAACACCAAGCCAGCTCCCCGGAAGCAAACTCCTAACATTTCTTGGCAGGGAAC
AGGCCAAGTGATCTACAAGGTTTCTATTTTTTATAAACCAGCAACTTCTAATGAGATAAT
CAAATATAAAGCTGCAAGAGGAGCTGTGGAAGATCGAATGCTGCTCCAGGAGGGGTAGGCCG
AGCATTGGTTTACAGCACTCCCCCTCAACTTACATTGACCTGGCTGTGGATGAGCATGGGCT
CTGGGCCATCCACTCTGGGCCAGGCCACCCATAGCCATTGGTTCTCACAAAGATTGAGCCGGG
CACACTGGGAGTGGAGCATTCATGGGATACCCCATGCAAGCCAGGATGCTGAAGCCCTCATT
CCTCTTGTGTGGGGTTCCTATGTGGTCTACAGTACTGGGGCCAGGGCCCTCATCGCATCAC
CTGCATCTATGATCCACTGGGCACTATCAGTGAGGAGGACTTGCCCAACTTGTCTCTCCCAA
GAGACCAAGAAAGTCACTCCATGATCCATTACAACCCAGAGATAAGCAGCTCTATGCTCGGAA
TGAAGGAAACAGAGATCATTTACAAACTCCAGACAAGAGAAAGCTGCCCTGGAAGTAAATGAT
TACAGCTGTGAGAAAGAGCACTGTGGCTTTGGCAGCTGTTCTACAGGACAGTGAGGCTATAGC
CCCTTACAATATAGTATCCCTCTAATCACACACAGGAAGAGTGTGTAAGAGTGGAAATACGT
ATGCCCTCCTTTCCCAAAATGTCACTGCCTTAGGTATCTTCCAAGAGCTTAGATGAGAGCATATC
ATCAGGAAAGTTTCAACAATGTCCATTACTCCCCAAACCTCCTGGCTCTCAAGGATGACCAC
ATTCTGATACAGCCTACTTCAAGCCTTTTGTFTTACTGCTCCCGAGCATTACTGTAACCTCTG
CCATCTTCCCTCCCACAATTAGAGTTGTATGCCAGCCCCATATTCACCACCTGGCTTTTCTC
TCCCTGGCCTTTTGTGAAGCTCTTCCCTCTTTTCAAATGTCTATTGATATTTCTCCATTTT
CACTGCCCACTAAAATACTATTAATATTTCTTTCTTTCTTTCTTTTGTGAGACAAGGT
CTCACTATGTTGCCAGGCTGGTCTCAAACCTCCAGAGCTCAAGAGATCCTCCTGCCTCAGCCT
CCTAAGTACCTGGGATTACAGGCATGTGCCACCACACCTGGCTTAAATACTATTTCTTATTG
AGGTTTAACTCTATTTCCCTTAGCCCTGTCTTCCACTAAGCTTGGTAGATGTAATAATAAA
GTGAAATATTAACATTGAAATATCGCTTTCCAGGTGTGGAGTGT'TPGCATCATTTGAATTC
TCGTTTCACTTTTGTGAACATGCAAGCTTTTACAGCTGTCAATTCATAGAGTTTAGGTGAGT
AACACATTAACAAGTGAAGATACAGCTAGAAAAATACTACAATCCCATAGTTTTTCCATGT
CCCAAGGAAGCATCAAAACGTATGTTTGTTCACCTACTCTTATAGTCAATGCGTTTCATCGTT
TCAGCCTTAAAAATATAGTCTGTCCCTTTAGCCAGTTTTCATGTCTGCACAAAGACCTTTCAAT
AGGCCTTCAAAATGATAATTCCTCAGAAAACCAAGCTAAGGGTGAGGACCCCAACTCTAGCC
TCTCTTGTCTTGTCTGTCTCTGTTTCTCTCTTCTGCTTTAAATTAATAAAAGTGACACTG
AGCAAAAAAAAAAAAAA

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FIGURE 468

MMVALRGASALLVLFLAAFLPPPQCTQDPAMVHYIYQRFVLEQGLEKCTQATRAYIQEFQEF
SKNISVMLGRCQTYTSEYKSAVGNLALRVERAQREIDYIQYLREADECIVSEDKTLAEMLLQE
AEEKKIRTLNASC DNMLMGIKSLKIVKKMMDTHGSWMKDAVYNSPKVYLLIGSRNNTVWEF
ANIRAFMEDNTKPAPRKQILTLWQGTGQVIYKGFLFFHNQATSNEIIKYNLQKRTVEDRMLL
PGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEPGLGVEHSWDTPCRSQ
DAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLFFPKRPRSHSMIHYNPRDK
QLYAWNEGNQIIYKLQTKRKLPLK

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FIGURE 469

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGGC
AGTGTTTTGCCTTACCCCAAGTGACCATGAGAGGTGCCACGCGAGTCTCAATCATGCTCCTC
CTAGTAACTGTGTCTGACTGTGTGTGATCACAGGGGCCCTGTGAGCGGGATGTCCAGTGTGGG
GCAGGCACCTGTCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGACCCCGCTGGGG
CGGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCCCCCTTCTTCAGGAAACGCAAGCAC
CACACCTGTCTTGTCTTGCCCAACCTGTCTGTGCTCCAGGTTCGCCGACGGCAGGTACCGCTGC
TCCATGGACTTGAAGAACATCAATTTTTAGGCGCTTGCCTGGTCTCAGGATACCCACCATCCT
TTTCTGAGCACAGCCTGGATTTTTATTTCTGCCATGAAACCCAGCTCCCATGACTCTCCAG
TCCCTACACTGACTACCCGTGATCTCTCTTGTCTAGTACGCACATATGCACACAGGCAGACATA
CCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTACAGCTTGAGGCTGTGGTGTG
AAAGGTGGCCAGCCTGGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTAAATGGCAGAAA
GGACATTCCCCCTCCCCCTCCCAGGTGACCTGCTCTCTTTCCTGGGCCCTGCCCTCTCCCCA
CATGTATCCCTCGGTCTGAATTAGACATTCTGGGCACAGGCTCTGGGTGCATTGCTCAGAG
TCCCAGGTCTTGGCCTGACCCCTCAGGCCCTTCACGTGAGGTCTGTGAGGACCAATTTGTGGGT
AGTTCACTCTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGACTCAAGATTGGTCTT
CCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCAGGGAGGCCAATCAGCC
CCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTTGTGGCCTGTGACCTGTGACCTTCTGCCA
GAATTGTCATGCCTCTGAGGCCCCCTCTTACCACACTTTACCAGTTAACCCTGAAGCCCCCA
ATTCCACAGCTTTTCCATTAAATGCAAAATGGTGGTGGTTCAATCTAATCTGATATTGACAT
ATTAGAAGGCAATTAGGGTGTTCCTTAAACAACCTCTTTTCCAAGGATCAGCCCTGAGAGCAG
GTTGGTGACTTTGAGGAGGGCAGTCTCTGTCCAGATTGGGGTGGGAGCAAGGGACAGGAGC
AGGGCAGGGGCTGAAAGGGGCACTGATTAGACCAGGGAGGCAACTACACACCAACATGCTGG
CTTTAGAATAAAAGCACCAACTGAAAAAA

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FIGURE 470

MRGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEETCHPG
SHKVPFFFRKRKHHHTCPCLPNLLCSRFPDGRYRCMDLKNINF

Important features:

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

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FIGURE 471

AGCGCCCGGGCGTCGGGGCGGTAAAAGGCCGGCAGAAAGGGAGGCACCTTGAGAAATGTCTTTCC
TCCAGGACCCCAAGTTTCTTCACCATGGGGATGTGGTCCATTGGTGACAGGAGCCCTGGGGGCTG
CTGCCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTTCTGTCCAAGCCCCAGAAAGCGCCCC
TGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTCAAAGCAA
AGGAGCTATGGGAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTTCTCTCT
GTCGAGAGGAAGCTGCGGATCTGTCCCTGCCCTGAAAAGCATGTTGGACCAGCTGGGCGTCCCCC
TCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTATTTCAAAG
GAGAAATCTTCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGCGGAAGATGATGTTTA
TGGGATTTATCCGTCTGGGAGTGTGGTACAACCTTCTCCGAGCCTGGAACGGAGGCTTCTCTG
GAAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTCGTGGTGGGATCAGGAAAGCAGG
GCATTCTTCTTGAGCACCAGAGAAAAAGAATTGGAGACAAAGTAAACCTACTTTCTGTTCTGG
AAGCTGCTAAGATGATCAAACACAGACTTTGGCCTCAGAGAAAAAATGATTGTGTGAAACTG
CCCAGCTCAGGGATAACCAGGGACATTCACCTGTGTTTCATGGGATGATTGTTTCCACTCGTG
TCCCTAAGGAGTGAGAAACCCATTTATACTCTACTCTCAGTATGGATTATTAATGTATTTTAA
TATTCTGTTTAGGCCCCTAAGGC AAAATAGCCCCAAAACAAGACTGACAAAAATCTGAAAAA
CTAATGAGGATTATTAAGCTAAAACCTGGGAAATAGGAGGCTTAAAATTGACTGCCAGGCTGG
GTGCAGTGGCTCACACCTGTAATCCAGCACTTTGGGAGGCCAAGGTGAGCAAGTCACTTGAG
GTCGGGAGTTCGAGACCAAGCCTGAGCAACATGGCGAAACCCCGTCTCTACTAAAAATACAAAA
ATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCAGCTACCCGGGAGGCTGAGGCAGGAGAA
TCACTTGAACCTGGGAGTGGAGGTTGCGGTGAGCTGAGATCACACCACTGTATTCCAGCCTG
GGTGA CTGAGACTCTAACTAA

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FIGURE 472

MSFLQDPSFFTGMWSIGAGALGAAALALLANTDVFLSKPQKAALEYLEDIDLKTLKEPRT
FKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSM LDQLGVPLYAVVKEHIRTEVKDFQP
YFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGWYNFFRAWNGGFSGNLEGE GFILGGVFVVG S
GKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

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FIGURE 473

AATATATCATCTATTTATCATTAAATCAATAATGTATTCTTTTATTCCAATAACATTGGGTTT
TGGGATTTTAAATTTTCAAACACAGCAGAAATGACATTTTTTCTGTCACTATTATTATTGTTGGT
ATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCTATC
AAGAAATAAAGAGAACCACAGTCAACCACACAATCATCTTTAGAAGACAGTGTGACTCCTAC
CAAAGCTGTCAAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGAGGGTT
AATTCTTGTTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATGATTGTA
AATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATATATACAA
TAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACTTTATTAAT
TTTTAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGATCATATAAT
TTGATACAAATAAAAGAAAAGTGTCTCTCCCTTACAGAATTGACATTTTAAATGCGATACA
GTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAAAGAAGGGAAAA
TGTTGCCAAGGAAAAAAAAA

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FIGURE 474

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGKG
IVKGRNLDSRGLILGAEAWGRGVKKNT

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FIGURE 475

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGTCTGCTGTACCAAGAGCTGGAGACACCAT
CTCCCACCGAGAGTCAATGGCCCCATTGGCCCTGCACCTCTCGTCTCGTCCCCATCCTCCTC
AGCCTGGTGGCTCCAGGACTGGAAGGCTGAACGCAGCCAAGACCCCTTCGAGAAATGCATG
CAGGATCCTGACTATGAGCAGCTGCTCAAGGTGGTGACCTGGGGGCTCAATCGGACCCTGAAG
CCCCAGAGGGTGATTGTGGTTGGCGCTGGTGTGGCCGGGCTGGTGGCCGCCAAGGTGCTCAGC
GATGCTGGACACAAGGTACCATCTCTGGAGGCAGATAACAGGATCGGGGGCCGCATCTTCACC
TACCGGGACAGAACACGGGCTGGATTGGGGAGCTGGGAGCCATGCGCATGCCAGCTCTCAC
AGGATCCTCCACAAGCTCTGCCAGGGCCTGGGGCTCAACCTGACCAAGTTACCCAGTACGAC
AAGAACACGTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAGAAGGTGCCC
GAGAAGCTGGGCTACGCCTTGCGTCCCCAGGAAAAGGGCCATCGCCCCGAAGACATCTACCAG
ATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGCACTGGGCTGCAGAAAGGCGATGAAGAAG
TTTGAAGGCACACGCTCTTGGAATATCTTCTCGGGGAGGGGAACCTGAGCCGGCCGGCCGTG
CAGCTTCTGGGAGACGTGATGTCCGAGGATGGCTTCTTCTATCTCAGCTTCGCCGAGGCCCTC
CGGGCCACACGCTGCCTCAGCGACAGACTCCAGTACAGCCGCATCGTGGGTGGCTGGGACCTG
CTGCCGCGCGCTGCTGAGCTCGCTGTCCGGGCTTGTGCTGTTGAACGCGCCCGTGGTGGCG
ATGACCCAGGGACCGCACGATGTGCACGTGCAGATCGAGACCTCTCCCCGGCGCGGAATCTG
AAGGTGCTGAAGGCCGACGTGGTGTGCTGCTGACGGCGAGCGGACCGCGGTTGAAGCGCATCACC
TTCTCGCCGCGCGCTGCCCGCCACATGCAGGAGCGCTGCGGAGGCTGCACTACGTGCCGGCC
ACCAAGGTGTTCTTAAGCTTCCGAGGCCCTTCTGGCGCGAGGAGCACATTGAAGGCGGCCAC
TCAAACACCGATCGCCGCTCGCGCATGATTTTCTACCCGCGCGCGCGAGGGCGCGCTGCTG
CTGGCCTCGTACACGTGGTGGACGCGGCGGCAGCGTTGCGCGGCTTGAGCCGGGAAGAGGCG
TTGCGCTTGGCGCTCGACGACGTGGCGGCATTGCACGGGCCGTGCTGCGCCAGCTCTGGGAC
GGCACCGGCGTCTGAAGCGTTGGGCGGAGGACACAGCACAGGCGGGTGGCTTTGTGGTACAG
CCGCCGGCGCTCTGGCAAACGAAAAGGATGACTGGACGGTCCCTTATGGCCGCATCTACTTT
GCCGCGAGCACACCGCTACCCGCACGGCTGGGTGGAGACGGCGGTCAAGTCGGCGCTGCGC
GCCGCCATCAAGATCAACAGCCGGAAGGGGCTGCATCGGACACGGCCAGCCCCGAGGGGCAC
GCATCTGACATGGAGGGGAGGGGCATGTGCATGGGGTGGCCAGCAGCCCTCGCATGACCTG
GCAAAGGAAGAAGGCAGCCACCTCCAGTCCAAGGCCAGTTATCTCTCCAAAACACGACCCAC
ACGAGGACCTCGCATTAAAGTATTTTCGGAAAAA

AA

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FIGURE 476

MAPLALHLLVLPILLSLVASQDWAERSQDPFEKCMQDPDYEQLLKVVVTWGLNRTLKPQRVI
VVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRILHK
LCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPEKLGVALRPQEKGHSPEDIYQMALNQ
ALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMSDGGFFYLSFAEALRAHSC
LSDRLQYSRIVGGWDLLEPRALLSSLSGLVLLNAPVVAMTQGGPHDVHVQIETSPPARNLKVLKA
DVVLLTASGPAVKRITFSPLPRHMQEALRRLHYVPATKVFLSFRFPFWREEHIEGGHSNTDR
PSRMIFYPPREGALLASYTWSDAAAAFAGLSREEALRLALDDVAALHGPVVRQLWDGTGVV
KRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKSALRAAIKI
NSRKGPSADTASPEGHASDMEGQGHVHGVASSPSHDLAKEEGSHPPVQGQLSLQNTTHTRTSH

Important features:**Signal peptide:**

amino acids 1-21

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FIGURE 477

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCCGGGCTTCTGCCTGCAT
 GGCAGCTCTGAAGCCACCCCTGTCTCTGGAGGACCCAGCAGGCGAGGGAAGAGGACAGGGAGCTCGGTGGGCGAGGAA
 GAATCAGAGCCGGGAAGCCGCCATCTACTAGAAGCATGAGAGATCGCGGCCCTCTCGAGGGGTCTCAATTTGCTT
 GCTGCTGTTCCAGAAAGATGCTTTTATCTTTAACTTTTGTGTTTCCCACTCTCCGACCCCGCGGTGATCTGCAT
 TCTGACATTTTGAGCTGGCATCTCTTGTGGCTGATCACCAGACCTCAACCGCTCTTACCTCTTCTTGACCTGAA
 CAACTAGCTCTGIGGGAATTTAGGGAGGAGCAGCAGGAAGGGGCTTCCCAAGAAACAAATGACCTTAACAGTTGCTG
 CTCTCAGATGCCAAGACTATGATGAGGTTTCCAAAGAGGACTCGCTGTGTCTGACAATGGGCCCTGTCTGGG
 ATATAGAAAAACCAAGCCAGCCCTACAGATGGCTATCTTACAAACAGGTTCTGATAGACAGAGTACTCTGGGTTCT
 CTGTCTCTTGCAATAAAGGTTATAAATCATCACCAGACCAGTTTGTCCGCTATCTTGTCTCAGAAATAGGCCAGAGTG
 GATCATCTCCGAATTTGGCTTGTACACGTACTCTATGGTAGCTGTACCTCTGTATGACACCTTTGGGACAGAAAGC
 CATCGTACATATTGTCAACAGGCTGATATGCCATGGTGATCTGTGACACACCCCAAAGGCATTTGGTGCTGAT
 AGGGAACTGAGAGAAAGGCTTCAACCCGAGCCTGAAGGTGATCATCTTATGGACCCCTTTGATGATGACCTGAA
 GCAAGAGGGGAGAAAGAGTGAATTTAGATCTTATCCCTATATGATGCTGAGAACCTAGGCAAGAGACACTTCAG
 AAAACCTCTGGCTCTTAGCCCCAGAAGACCTGAGCGTCACTGCTTCAACAGTGGGACCAAGGTGACCCCAAAGG
 AGGCTATGATAACCCATAAAATATTTGTTCAAATGCTGCTGCCCTTCTCAAATGTGTGGAGCATGCTTATGAGCC
 CACTCTGATGATGTGGCCATATCTTACCTCCCTCTGGCTCATATGTTTGAAGGATTTGACAGGCTTGTGTTGTA
 CAGCTCTGGAGCCAGAGTTGGATTCTTCCAAGGGATATTCGGTTGTCTGGCTGAGCAGATCAAGACTTTGAAGCC
 CACATTTGTTCCCGCGGTGCTCGACTCCTTAACAGGATCTACGATAAGGTACAATAAGAGGCCAAGACCCCTT
 GAAGAAGTTCTGTTGAAGCTGCTGTTTCCAGTAAATCAAAGAGCTTCAAAGGGGTATCATCAGGCATGATAG
 TTTCTGGGACAAGCTCATCTTTGCAAGATCCAGGACAGCCTGGGCGGAAGGGTTCTGTGTAATTGCTACTGGAGC
 TGCCCCATGTCCACTTTCAGTCATGACATCTTCCGGGACGCAATGGGATGTCAGGTGATGAAGCTTATGCTCA
 AACAGAATGCACAGGTGGCTGTACATTTACATTTACCTGGGACTGGACATCAGGTCACTTGGGGTGGCCCTGGC
 TTGCAATTACGTGAAGCTGGAAGATGTGGCTGACATGAACACTTTACACTGAATTAATGAAGGAGAGGTCTGCAT
 CAAGGTTCAAAAGCTGTTCAAAGGATACCTGAAGGACCCCTGAGAAGACACAGGAAGCCCTGGACAGTGATGGCTG
 GCTTACACAGAGACATTTGGTCTGGCTGCCGAATGGAACTCTGAAGATCATCGACCTAAAAAGAACATTTT
 CAAGCTTGGCCCAAGGAGAAATACATTTGCCACCGAGAAGATAGAAATATCTACAACAGGAGTCAACCGATTTACA
 AATTTTGTACACGGGGAGAGCTTACGGTCATCTTTAGTAGGAGTGGTGTCTCTGACACAGTACTACTTCCCTC
 ATTTGACGCCAAGCTTTGGGGTGAAGGGCTCCTTTGAGGAACTGTGCCAAACCAAGTTTGAAGGGAAGCCATTT
 AGAAGACTTGCAGAAAAATTTGGGAAGAAAGTGGGCTTAAACCTTTTGAACAGGTCAAAGGCCATTTTCTCATCC
 AGAGCCATTTTCCATTGAAATGGGCTTGTGACACCACCATTTGAAGCAAGAGGAGGAGAGCTTTCCAAATACTT
 TCGGACCCAAATTTGACAGCCTGTATGAGCAGATCCAGGATAGGATAAGGTACTTAAAGTACCTGCCGGCCACTG
 TGCATCTGCTGTGAGAAAATGGATTAACAACTATTCTTACATTTGTTTGGCTTCTCCTCATTTTTTTTAAAC
 TGTTTAACTCTAAAGCCATAGCTTTTGTGTTTATATTGAGACATATAATGTGTAACCTTAGTTCCTCAATAAATCA
 ATCCTGTCTTCCCATCTTCGATGTTGCTAATATTAAGGCTTCAGGGCTACTTTTATCAACATGCCTGTCTCAA
 GATCCAGTTTATGTTCTGTGCTCTTCTCATGATTTCACAACTTAATACTATTAGTAACCAAGTCTCAAGGTT
 CAAAGGACCCCTTGTGCTCTTCTTGTGTTGTTGATAAACTAACTTGCCAAAGCTCTCTAGTCTTATTACA
 TCTTCTACTGTTCAAACCTAAGAGATTTTAAATTTCTGAAAACTGCTTACAAATTCATGTTTCTAGCCACTCCAC
 AAACCACTAAAAATTTAGTTTATGCTATCACTCATGTCAATCATATCTATGAGACAAATGTCTCCGATGCTCTT
 CTGGCTAAATTAATTTGTGTACTGAAGGGAAGAGTTTGTATCATACCAACATCTTCAATCTCTCTAGTTAGATA
 TCTGACTTGGGAGTATTAATAATTTGGGTCTATGACATACCTTCCAANAAGGAATGCTGTCTTAAAGCATTAITTA
 CAGTAGGAACCTGGGAGTAAATCTGTTCCTACAGTTTCTGCTGAGCTGAGCTGTGGGGGAAGGAGTTGACA
 GGTGGGCCAGTGAACCTTTCCAGTAAATGAAGCAAGCACTGAATAAAACCTTCTTGAACCTGGGAACAAAGATCT
 ACAGGCAAGCAGATGGCCACACAAAGCAGGCTTATTTCTGTGAAGGAACCAACTGCTTCCCCACCTCTGGATT
 AGAGTCTCTGCTTCACTTACCCACAGATAACACATGTTGTTTCTACTTGTAAATGTAAGTCTTTAAATAAAC
 TATTACAGATAAAAA

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FIGURE 478

MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNFLLLFTKMLFI FNF
LFSPLPTPALICILTFGAAIFLWLITRPQPVLPDLLNNQSVGIEGGARKGVSQKNNDLTSCC
FSDAKTMYEVFQRLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYSKSPDQ
FVGIFAQNRPEWIISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKALVLIG
NVEKGFTPSLKVIIIMDPFDDDLKQGEKSGIEILSLYDAENLGKEHFRKPVPPSPEDLSVIC
FTSGTTGDPKGAMITHQNIIVSNAAFLKCEHAYEPTPDDVAISYLP LAHMFERIVQAVVYSC
GARVGFFQGDIRLLADDMKTLKPTLFPAPVRLNRIYDKVQNEAKTPLKKFLLKLA VSSKFKE
LQKGIIRHDSFWDKLIFAKIQDSLGGRRVRVIVTGAAPMSTSVMTFFRAAMGCQVYEAYGQTEC
TGGCTFTLPGDWTSGHVGVPACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFKGYLKDPEKT
QEALDSDGWLHTGDIGRWLPNGTLKIIDRKKNIFKLAQGEYIAPEKIENIYNRSQPV LQIFVH
GESLRSSLVGVVVPD TDVLP SFAAKLGVKGSFEELCQNQVVREAILEDLQKIGKESGLKTFEQ
VKAIFLHPEPFSIENGLLPTLKA KRGE LSKYFRTQIDSLYEHIQD

Important features:**Type II transmembrane domain:**

amino acids 61-80

Putative AMP-binding domain signature.

amino acids 314-325

N-glycosylation site.

amino acids 102-105, 588-591 and 619-622

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FIGURE 479

GGAGGCGGAGGCCGCGGCGAGCCGGGCCGAGCAGTGAGGGCCCTAGCGGGGCCGAGCGGGGC
CCGGGGCCCCCTAAGCCATTCTGAAGTCATGGGCTGGCCAGGACATTGGTGACCCGCCAATCC
GGTATGGACGACTGGAAGCCAGCCCCCTCATCAAGCCCTTTGGGGCTCGGAAGAAGCGGAGC
TGGTAGCTTTACCTGGAAGTATAAACTGACAAACCAGCGGGCCCTCGGAGATTTCTGTACAGACA
GGGGCCGTGCTTTTCTGCTGGTGACTGTCATTGTCAATATCAAGTTGATCTGGACACTCGG
CGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGCCCTAGGC
CGCTCGAGGCCCCACGCGGCAGAGGCACTGGTCCCCGGCGGGTCTGGAGCTGAGAGGTGTAT
TCAAGTCGCGAGCAAAGTATATGTGGCAGTGGATGGCACCACGGTGCTGGAGGATGAGGCCCGG
GAGCAGGGCCGGGGCATCCATGTCTATGTCTCAACCAGGCCACGGGCCACGTGATGGCAAAA
CGTGTGTTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTGCTATTCCCTCAACATGGTA
GCGCCCGGGCCGAGTGCTCATCTGCATGTCAAGGATGAGGGCTCCTTCCACCTCAAGGACACA
GCCAAGGCTCTGCTGAGGAGCCTGGGCAGCCAGGCTGGCCCTGCCCTGGGCTGGAGGGACACA
TGGGCCCTTCGTGGGACGAAAAGGAGGTCTGTCTCGGGGAGAAACATTCTAAGTCACTGCC
CTCTCTCTCTGGGGGACCCAGTCTCTGCTGAAGACAGATGTGCCATTGAGCTCAGCAGAAGAG
GCAGAGTGCCATCGGCAGACACAGAGCTGAACCGTCGCGCCGGCGCTTCTGCAGCAAAGTT
GAGGGCTATGGAAGTGTATGCAAGCTGCAAGGACCCACACCATTCAGTTTCAAGCTGACCCCA
CTCCCAGACAACAAGGTCTCTCAATGTGCCTGTGGCTGTCTTGCAGGGAACCGACCCAATTAC
CTGTACAGGATGCTGCGCTCTCTGCTTTAGCCCCAGGGGGTGCTCTCTCAGATGATAACAGTT
TTCATGACGGCTACTATGAGGAACCCATGGATGTGGTGACCTGTGTTGGTCTGAGGGGCACTC
CAGCATACTCCATCAGCATCAAGAATGCCCGCTGTCTCAGCACTACAAGGCCAGCCCTCACT
GCCACTTTCAACCTGTTTCCGGAGGCCAAGTTTGCTGTGGTTCTGGAAGAGGACCTGGACATT
GCTGTGGATTTTTCAGTTTCTGAGCCAATCCATCCACCTACTGGAGGAGGATGACAGCCTG
TACTGCATCTCTGCTGGAATGACCAGGGGTATGAACACACGGCTGAGGACCCAGCACTACTG
TACCGTGTGGAGACCATGCCCTGGGCTGGGCTGGGTGCTCAGGAGGTCCTTGTAAGAAGGAGGAG
CTTGAGCCCAAGTGGCCTACACCGGAAAAGCTCTGGGATTGGGACATGTGGATGCGGATGCCCT
GAACAACGCCGGGGCCGAGAGTGATCATCCCTGACGTTTCCCGATCCTACCACCTTTGGCATC
GTCGGCCTCAACATGAATGGCTACTTTCACGAGGCCCTACTTCAAGAAGCACAGTTTCAACACG
GTTCCAGGTTCCAGTACAGGAATGTGGACAGTCTGAAGAAAGAAGCTTATGAAGTGGAGATT
CACAGGCTGCTCAGTGAGGCTGAGGTTCTGGACCACAGCAAGAACCCTTGTGAAGACTCTTTC
CTGCAGACACAGAGGGCCACACCTACCTGCGCTTTATTCCAATGGAGAAAGATGATGACTTC
ACCACCTGGACCCAGGTTGCCCAGTGCCTCCATCTCTGGGACCTGGATGTGCGTGGCAACCCT
CGGGGCTGTGGAGATTGTTTTCGGAAGAAGAACCACTTCTGTTGGTGGGGGTCCCGGCTTCC
CCCTACTCAGTGAAGAAGCCACCTCAGTACCCCAATTTCTCTGGAGCCACCCCAAGGAGG
GAGGAGTCCCGCAGGAGCCCAAGAACAGACATGAGACCTCTCCAGGACCTGCGGGGCTGGGT
ACTGTGTACCCCGAGGCTGGCTAGCCCTTCCCTCCATCTGTAGGATTTTGTAGATGCTGGTA
GGCGCTGGGCTACCTTGTTTTAAACATGAGACTTAATTACTAATCCAAGGGGAGGGTCCC
CTGCTCCAAGCCCGCTTCTGAGTTAAAAGTCTATTTTATTACTTCTTCTGTTGGAGAAGGGC
AGGAGACTACCTGGGAATCATTACGATCCCTAGCAGCTCATCTGCCCTTGAATACCCCTCAC
TTTCCAGGCTGGCTCAGAACTCAACCTATTTATTGACTGTCTGAGGCTTGAAGGCTTGAACAGGC
CGAACCTGGAGGGGCTGGATTCTTTTGGGCTGGAAATGCTGCCCTGAGGGTGGGGCTGGCTC
TTACTCAGGAACATGCTGTGCCCAACCCATGGACAGGCCACGCTGGGGCCCAACATGTGACAC
AGACTACTCAGAGACCTTAGACACTGGACAGGCCCTCCTCTCAGCCTTCTCTTGTGCCAGA
TTTCCAAGCTGGATAAGTTGGTCATTGATTAAAAAAGGAGAAGCCCTCTGGGAAAAAAAAA
AAAAAAAAAAAAAAAAA

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FIGURE 480

MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQALRRFCQTGAVLFLLVTIVINIKLILDTRR
AISEANEDPEPEQDYDEALGRLEPPRRRGSGPRRVLDEVYSSRSKVYVAVDGTTVLEDEARE
QGRGIHVIVLNQATGHVMAKRVFDITYSPHEDEAMVLF LNMVAPGRVLICTVKDEGSFHLKDTA
KALLRSLGSQAGPALGWRDTWAFVGRKGGPVFGEKHSKSPALSSWGDVPVLLKTDVPLSSAEEA
ECHWADTELNRNRRRFRFC SKVEGYGSVCCKDPTPIEFSPDPLPDNKVLNVPVAVIAGNRPNYL
YRMLRSLLSAQGVSPQMITVFIDGYEPMQDVVALFGLRGIQHTPISIKNARVSQHYKASLTA
TFNLFPEAKFAVLEEDLDIAVDFFSFLSQSIHLEEDDSLYCISAWNDQGYEHTAEDPALLY
RVETMPGLGWVLRRLSLYKEELEPKWPTPEKLWDWDMWMMRMEQRRGRECIIPDVSRSYHFGIV
GLNMNGYFHEAYFKKKHFNTVPGVQLRNVDLSLKEAYEVEVHRLLSAEVLDHSKNPCEDSFL
PDTEGHTYVAFIRMEKDDDFTTWTQLAKCLHIWDLVVRGNHRLGLWRLFRKKNHFLVVGVPASP
YSVKKPPSVTPIFLEPPKKEGAPGAPEQT

Important features:**Transmembrane domain:**

amino acids 38-55

Homologous region to Mouse GNT1

amino acids 229-660

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FIGURE 481

GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTGCTGAACTCTGTCAACCA
GGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT
GCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAAGTT
CCCAACAGAGAAGCAACAGAAAATTTCCCATGTCTACTTTTGCAATGTAACCCAGAGGGTATCA
TTCGTGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCTGCTGTTGAGGTGCAATCA
GCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACTCTGGAA
TTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTGGATTATT
ATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTATCAGGGATC
TGGCAACGTAGAAGAAAAGAACAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAA
AACATGATCACAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGGGGGCATATTA
ATGATGCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTC
CTCAAGAAATTAAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATACCAAGAGCAGAT
CATATATTTTGTTTTACCATTCTTCTTTTGAATAAATTTTGAATGTGCTTGAAAGTGAAAAG
CAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTACGACTCAAAATATTCTAA
AATATTTTCTGACAGTATAGTGATAAATGTGGTCATGTGGTATTTGTAGTTATTGATTTAA
GCATTTTGTAGAAATAAGATCAGGCATATGTATATATTTTACACTTCAAAGACCTAAGGAAAA
ATAAATTTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTTT
TGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTA
AATGGATGGATAAAAATGGAATTACTCATATACAGGGTGAATTTTATCCTGTTATCACACCA
ACAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGACAATTCTATTGTGGACCATT
TCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTTAA
AAAAAAAAAAAAAAAAAAAAA

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FIGURE 482

MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVPN
REATEISHVLLCNVTQRVSFWFVVTDPKSNHTLPAVEVQSAIRMNKNRINNAFFLNDQTLEFL
KIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPSEVDDAEDKCENM
ITIENGIPSDPLDMKGGILMMPS

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FIGURE 483

CGTCTCTGCGTTTCGCC**ATG**CGTCCCGGGGCGCCAGGGCCACTCTGGCCTCTGCCCTGGGGGGC
CCTGGCTTGGGCCGTGGGCTTCGTGAGCTCCATGGGCTCGGGGAACCCCGCGCCCGGTGGTGT
TTGCTGGCTCCAGCAGGGCCAGGAGGCCACTGCAGCCTGGTGCTCCAGACTGATGTACCCCG
GGCCGAGTGTGTGCCTCCGGCAACATTGACACCGCCTGGTCCAACCTCACCCACCCGGGGAA
CAAGATCAACCTCCTCGGCTTCTTGGGCCTTGTCCACTGCCTTCCCTGCAAGAGATCGTGCGA
CGGCGTGGAGTGC GGCCCGGGCAAGGCGTGCCGCATGCTGGGGGGCGCCCGCGCTGCGAGTG
CGCGCCCGACTGCTCGGGGCTCCCGGCGCGGCTGCAGGTCTGCGGCTCAGACGGCGCCACCTA
CGCGACGAGTGCGAGCTGCGCGCGCGCGCTGCCGCGCCACCCGGACCTGAGCGTCATGTA
CCGGGGCGCGTGCCGCAAGTCTGTGAGCACGTGGTGTCGCCCGGGCCACAGTCTGTCGTCGT
GGACACAGCGGGCAGCGCCCACTGCGTGGGTGCTGCGAGCGGCGCCCTGCCCTGTGCCCTCCAG
CCCCGGCCAGGAGCTTTCGGGCAACAAACAGCTCACCTACATCTCCTCGTGCCACATGCGCCA
GGCCACCTGCTTCTTGGGCGCGTCCATCGGCGTGCGCCACCGCGGGCAGCTGCGCAGGCCACCC
TGAGGAGCCGCCAGGTGGTGAGTCTGCAGAAGAGGAAGAGAACTTCGTG**TGA**GCCTGCGAGGAC
AGGCTTGGGCTGGTGCCCGAGGCCCCCATCATCCCTGTATTATTTATTTGCCACAGCAGAGTC
TAATTATATATGCCACGGACACTCCTTAGAGCCCGGATTTCGGACCCTTGGGGATCCCAGAACC
TCCCTGACGATATCCTGAAGGACTGAGGAAGGAGGAGGCTGGGCGCGGCTGGTGGGTGGGAT
AGACCTGCGTTCGGACACTGAGCGCCTGATTTAGGGCCCTTCTCTAGGATGCCCCAGCCCT
ACCCTAAGACCTATTGCCGGGGAGGATTCACACTTCCGCTCCTTTGGGGATAAACCTATTAA
TTATTGCTACTATCAAGAGGGCTGGGCATTCTCTGCTGGTAATTCCTGAAGAGGCATGACTGC
TTTTCTCAGCCCCAAGCCTCTAGTCTGGGTGTGTACGGAGGGTCTAGCCTGGGTGTGTACGGA
GGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGT
GAGTACGGAGGGTCTAGCCTGGGTGTGTATGGAGGATCTAGCCTGGGTGAGTATGGAGGGTCT
AGCCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGTGTATGGAGGGTCTAGCCTGGGTGAGTAT
GGAGGGTCTAGCCTGGGTGTGTATGGAGGGTCTAGCCTGGGTGAGTATGGAGGGTCTAGCCTG
GGTGTGTACGGAGGGTCTAGTCTGAGTGCGTGTGGGGACCTCAGAACAAGTGTGACCTTAGCCC
AGCAAGCCAGGCCCTTCTATGAAGGCCAAGAAGGCTGCCACCATTCCCTGCCAGCCCAAGAAGT
CCAGCTTCCCACATGCCTCTGTGTGCCCTTTGCGTCCGTGTGAAGGCCATTGAGAAATGCCCA
GTGTGCCCCCTGGGAAAGGGCACGGCTGTGCTCCTGACACGGGCTGTGCTTGGCCACAGAAC
CACCCAGCGTCTCCCTGCTGTGTCCACGTCAGTTTCATGAGGCAACGTCGCGTGGTCTCAGA
CGTGAGCAGCCAGCGGCAGCTCAGAGCAGGGCACTGTGTCCGCGGAGCGAAGTCCACTCTG
GGGAGGCTCTGGCGGGGACCCAGGGCCACTGCTCACCCACTGGCCCCGGGGGGGTGTAGACG
CCAAGACTCAGCATGTGTGACATCGGAGTCCCTGGAGCCGGGTGTCCCACTGGCACCACTAG
GTGCTGCTGCTCCCTCCACAGTGGGGTTACACCCAGGGCTCCTTGGTCCCCCACAACCTGCCCC
GGCCAGGCTCTCAGACCCAGACTCCAGCCAGACCTGCCTCACCCACCAATGCAGCCGGGGCTG
GGGACACCAGCCAGGTGCTGGTCTTGGGCCAGTTCTCCACAGACGGCTCACCCCTCCCTCCAT
CTGCGTTGATGCTCAGAATCGCTACCTGTGCGTGTAAACCAAGCCCTCAGAGCCTCAGACGACTA
TGGGGAGAGGACAAACAGGAGGATATCCAGCTTCCCCGGTCTGGGGTGAAGGAATGTGGGGAGC
TTGGGCATCTCTCCAGCCTCTCCAGCCCCAGGCAGTGCTTACCTGTGGTGCCAGAGAA
AGTGCCCCCTAGGTTGGTGGGTCTACAGGAGCCTCAGCCAGGCCACCCACCCCTGGGGCC
CTGCCTCACCAAGGAAATAAAGACTCAAGCCATAAAAAAA

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FIGURE 484

MRPGAPGPLWPLPWGALAWAVGFVSSMSGGNPAPGGVCWLQQGQEATCSLVLQTDVTRAEC
CA
SGNIDTAWSNLTHPGNKINLLGFLGLVHCLPCKDSCDGVCEGPGKACRMLGGRPRCECAPDCS
GLPARLQVCGSDGATYRDECELRAARCRGHPDLSVMYRGRCRKSCHEVVCPRPQSCVVDQTGS
AHCVCVRAAPCPVPSSPGQELCGNNNVTYISSCHMRQATCFLGRSIGVRHAGSCAGTPEEPPG
GESAEEEENFV

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation sites.

amino acids 73-77, 215-219

Osteonectin domain proteins.

amino acids 97-130, 169-202

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FIGURE 485

GCTCGAGGCCGGCGGGCGGGAGAGCGACCCGGGCGGCTCGTAGCGGGGCCCCGGATCCCC
GAGTGGCGGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGAGATGATGGGCTTGGGA
AACGGGCGTCGCAGCATGAAGTCGCGCCCCCTCGTGCTGGCGGCCCTGGTGGCCTGCATCATC
GTCTTGGGCTTCACTACTGGATTGCGAGCTCCCGAGCGTGGACCTCCAGACACGGATCATG
GAGCTGGAAGGCAGGGTCCGAGGGCGGCTGCAGAGAGAGGCGCCGTGGAGCTGAAGAAGAAC
GAGTTCCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAAATCCAGTCCAGCCACAAC
TTCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGCGGTTTGGTGAATAACATC
ACCACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCCTGCAGAGGAATTAC
GGCAGGCTGCAGCAGGATGTCTCCAGTTTCAGAAGAACCAGACCAACCTGGAGAGGAAGTTC
TCCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTGTGAGGAGCGA
ATAGAAGAGGTCAACAAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGAGTGAACAAC
GACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAGGCAGCAGGCCTG
CCACACACAGAGGTGCCACAAGGGAAGGGAACGTGCTTGGTAACAGCAAGTCCCAGACACCA
GCCCCAGTTCCGAAGTGGTTTTGGATTCAAAGAGACAAGTTGAGAAAAGAGGAAACCAATGAG
ATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAGCCAGGCCGGGAGCAG
GTGGTGAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGAGAACTGGGCCAGACC
CCACAGGTGCAGGCTGCCCTGTCAAGTGAAGCAGGAAAATCCAGAGATGGAGGGCCCTGAGCGA
GACCAGCTTGTTCATCCCCGACGGACAGGAGGAGGAGCAGGAAGCTGCCGGGAAGGGAGAAAC
CAGCAGAACTGAGAGGAGAAGATGACTACAACATGGATGAAAATGAAGCAGAATCTGAGACA
GACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAACATAGATGTTTTTAATGTTGAAGATCAG
AAAAGAGACACCATAAATTTACTTGTATCAGCGTGAAAAGCGGAATCATACACTCTGAATTGAA
CTGGAATCACAATTTTCAACAGGGCCGAAGAGATGACTATAAAATGTTTCATGAGGGACTGA
ATACTGAAAATGTGAAATGTACTAAATAAAATGTACATCTGA

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FIGURE 486

MMGLGNRRSMKSPPLVLAALVACIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAAERGAV
ELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQLKT
LQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVASRD
LSENNDQRQQLOALSEPQPRLOAAGLPFHTVEVPQGKGNVLGNSKSQTPAPSSEVVLDSCRQVEK
EETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQVQAALSVSQENPEM
EGPERDQLVIPDGQEEEQEAAGEGRNQQLRGEDDYNMDENEAESETDKQAALAGNDRNIDVF
NVEDQKRDTINLLDQREKRNHTL

Important features:**Signal peptide:**

amino acids 1-29

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FIGURE 487

AAC TCAA ACTCCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGAGTGGCCTTGGCAGGG
TGTTGGAGCCCTCGGTCTGCCCGCTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTCATGTTAT
GGCAAGAGCTCTACTCGTGCGGTGCTTCTTCTCCTTGGCATACAGCTCACAGCTCTTTGGCCT
ATAGCAGCTGTGGAAATTATACCTCCCGGTGCTGGAGGCTGTTAATGGGACAGATGCTCGG
TTAAATGCACCTTTCTCCAGCTTTGCCCTGTGGGTGATGCTCTAACAGTGACCTGGAATTTT
CGTCTCTAGACGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTCCAACCC
ATGAGTGGGCGGTTTAAGGACCGGTGTCTTGGGATGGGAATCCTGAGCGGTACGATGCCTCC
ATCCTTCTCTGGAACCTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGAAGAACCCA
CCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTACGCTTCTCT
GAGATCCACTTCTGGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCATAATAGTAATT
GTAGTGGTCTCTTCCAGCATACC CGAAAAAGCGATGGGCCGAAAGAGCTCATAAAGTGGTG
GAGATAAAATCAAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCTGTTTATTTAGAA
GACACAGACTTAACAATTTTAGATGGAAGCTGAGATGATTCCAAGAACAAGAACCCTAGTATT
TCTTGAAGTTAATGGAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGTTTCCAACCAAGTTC
TGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAGAGTGCTCCTCCATAT
CACCAGTCATACAGCCTCATTATTAAGGTCTTATTTAATTCAGAGTGTAATTTTTTCAA
GTGCTCATTAGGTTTTATAAACAAGAAGCTACATTTTGGCCCTTAAGACACTACTTACAGTGT
TATGACTTGTATACATATATTGGTATCAAAGGGGATAAAAGCCAATTTGTCTGTTACATTT
CCTTTCACGTATTTCTTTTAGCAGCACTTCTGCTACTAAAGTTAATGTGTTTACTCTCTTTCC
TTCCACATTTCTCAATTAAGGTGAGCTAAGCCTCCTCGGTGTTTCTGATTAACAGTAAATC
CTAAATTCAACTGTTAAATGACATTTTTATTTTTATGTCTCTCCTTAACATATGAGACACATC
TTGTTTTACTGAATTTCTTTCAATATTCAGGTGATAGATTTTTGTGCG

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FIGURE 488

MYGKSSTRAVLLLLGIQLTALWPIAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVTW
NFRPLDGGPEQFVFYYHIDPFQPMsGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQVK
NPPDVDGVIGEIRLSVVHTVRFSEIHFLALAIGSACALMIIIVVVVLFQHYRKKRWAERAHK
VVEIKSKEERLNQEKKVSVYLEDTD

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FIGURE 489

[illegible]

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FIGURE 490

MLLLWVSVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDFSFGRLTFHFGSQVVKLPPFINFM
KTRGTSFLNAYTNSPICCPSRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQKF
GKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPVMVNLIRNRTKVRVMERDQNTDKAVNWLRK
EAINYTEPFVIYLG LNLPHYPSPSSGENFGSSTFHTSLYWLEKVS HDAIKIPKWSPLSEMHP
VDYYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVYSSDHG
ELAMEHRQFYKMSMYEASAHVPLLMMGPGIKAGLQVSNVSLVDIYPTMLDIAGIPLPQNLSG
YSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYSDGASILPQLFD
LSSDPDELTNVAVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWKQSIGQYNSNVIA
NLRWHQDWQKEPRKYENAIQWLKTHMNPRAV

Important features:**Signal peptide:**

amino acids 1-15

N-glycosylation sites.amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,
498-501**Sulfatases proteins:**

amino acids 286-315, 359-369, 78-97

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FIGURE 491

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGA
GCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATG**GC
CTCTCTTGGCCTCCAACCTGTGTGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACTGGT
TGCCATGCTGCTCCCCAGCTGAAAAACAAGTTCTTATGTGCGTGCCAGCATTGTGACAGCAGT
TGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAGTGTGA
CATCTATAGCACCCCTTCTGGGCCTGCCCGCTGACATCCAGGCTGCCAGGCCATGATGGTGAC
ATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCACAGTCTT
CTGCCAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTCATCCTTGG
AGGCCTCCTGGGATTCTATCTGTTCCTGGAATCTTCATGGGATCCTACGGGACTTCTACTC
ACCACTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCCTCTTACTTGGGCATTATTTCT
TTCCCTGTCTCCTGATAGCTGGAATCATCCTCTGCTTTTCTGCTCATCCAGAGAAATCG
CTCCAATACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTCTCCAAGGCCTGG
TCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCTACAGCCTGACAGGGTATGTG**TGA**AGAAC
CAGGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAGCACCCCCGAGGGCCA
CAGGTGAGGGACACTACCACTGGATCGTGTGAGAAGGTGCTGCTGAGGATAGACTGACTTTGG
CCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAACAGCATGCAGGTTGAATTGCCAA
GGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCACCTTGCTGCTCCCTGCCCTAAGTCCCC
AACCTCAACTTGAAACCCCATTTCCCTTAAGCCAGGACTCAGAGGATCCCTTTGCCCTCTGGT
TTACCTGGGACTCCATCCCCAACCCACTAATCACATCCCAGTACTGACCTCTGTGATCAA
AGACCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGGGGATGGGAAGGAGAAGCAGT
GGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCCTCCAAAGAACTGATTGGCCC
TGGAACCTCCATCCCACTCTTGTTATGACTCCACAGTGTCCAGACTAATTTGTGCATGAAGT
AAATAAAACCATCTACGGTATCCAGGGAACAGAAAGCAGGATGCAGGATGGGAGGACAGGAA
GGCAGCCTGGGACATTTAAAAAATA

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FIGURE 492

MASLGLQLVGVIILGLLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQ
CDIYSTLLGLPADIQAAQAMMVTSSAIISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVFFI
LGGLLGFIPIVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSSQR
NRSNYDAYQAQPLATRSSPRGPQPPKVKSEFNSYSLTGYV

Important features:**Signal peptide:**

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

FMP-22 / EMP / MP20 family proteins.

amino acids 46-59

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FIGURE 493

GCACTGCTGCTGTCCCATCAGCTGCTCTGAAGCTCCATGGTGCCCAGAATCTTCGCTCCTGCT
TATGTGTCACTGTCTCCTCCTCTTGTGTCCAAGGGAAGTCATCGCTCCCCTGGCTCAGAA
CCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAGTGC
TGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCTGCACCTTC
TGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCCCTTTGGCCTCACAAACGATTTTGTGTGAAG
CTGAAGGTTCAAGGTGTGAATTCCCAGTGCCACTCATCTCCCATCTCCAGTAAATGTGAAAGC
AGAAGACGTTTTCCCTTGAGAAGACATAGAAAGAAAATCAACTTTCACTAAGGCATCTCAGAAA
CATAGGCTAAGGTAATATGTGTACCAGTAGAGAAGCCTGAGGAATTTACAAAATGATGCAGCT
CCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGTAGATTATCA
GGAAATAAATAAAGTGGTTTTTCCAATGTACACACCTGTAAAA

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FIGURE 494

MVPRIFAPAYVSVCLLLCPREVIAPAGSEPWLCQPAPRCGDKIYNPLEQCCYNDAIVSLSET
RQCGPPCTFWPCFELCCLDSFGLTNDFFVVKLVQGVNSQCHSSPISSKCESRRRFP

Important features:

Signal peptide:

amino acids 1-25

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FIGURE 495

CTCCACTGCAACCAACCCAGAGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATTT
TCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCTGA
TGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCTGCAGCACTGTTGCT
ATGATGATGCCGTCGTGCCCTTGCCAGGACCCAGACGTGTGGAACTGCACCTTCAGAGTCT
GCTTTGAGCAGTGTGCCCTTGACCTTCATGGTGAAGCTGATAAACAGAACTGCGACTCAG
CCCGGACCTCGGATGACAGGCTTTGTGCGAGTGTCAGCTAATGGAACATCAGGGGAACGATGA
CTCCTGGATTCTCCTTCCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTACCTGAGATCTGGGA
TGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTCAACTGCCCCACTTCATTCTGTGACC
TGCTCTGAGGCCACCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTTCTAGAATTCTGGA
CAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCTCCTGATGACCCCTATG
GCCAACATCAACCCGGCACCACCCCAAGGCTGGCTGGGGAACCCTTCACCTTCTGTGAGATT
TTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAATAAATTTATGTA
CTTTATAAATGAAAA

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FIGURE 496

MAPRGCI VAVFAIFCISRLLC SHGAPVAPMTFYLMLCQPHKRCGDKFYDPLQHCCYDDAVVPL
ARTQT CGNCTFRVC FEQCCPWTFMVKLINQNCD SARTSDDRLCRSVS

Important features:

Signal peptide:

amino acids 1-24

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FIGURE 497

TGAAGGACTTTTCCAGGACCCAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCACTC
CTTGGGCTCCGCAGCCGATCACATGAAAGGTGGTGCCAAGTCTCCTGCCTCCTCGTCTCCTGGC
ACAGGTGTGGCTGGTACCCGGCTTGGCCCCAGTCTCAGTCGCCAGAGACCCAGCCCCCTCA
GAACCAGACCAGCAGGGTAGTGCAGGCTCCAGGGAGGAAGAGGAAGATGAGCAGGAGGCCAG
CGAGGAGAAGGCCGGTGAGGAAGAGAAAGCCTGGCTGATGGCCAGCAGGCAGCAGCTTGCCAA
GGAGACTTCAAACCTCGGATTAGCCCTGCTGCGAAAGATCTCCATGAGGCACGATGGCAACAT
GGTCTTCTCTCCATTGGCATGTCCCTTGGCCATGACAGGCTTGATGCTGGGGGCCACAGGGCC
GACTGAACCCAGATCAAGAGAGGGCTCCACTTGAGGCCCTGAAGCCCACCAAGCCCGGGCT
CCTGCCTTCCCTCTTTAAGGGACTCAGAGAGACCTCTCCCGCAACCTGGAACCTGGGCCCTCTC
ACAGGGGAGTTTTGCCTTCATCCACAAGGATTTTGATGTCAAAGAGACTTTCTTCAATTTATC
CAAGAGGTATTTGATACAGAGTGCCTGCTATGAATTTTCGCAATGCCTCACAGGCCAAAAG
GCTCATGAATCATTACATTAACAAAGAGACTCGGGGAAAATTTCCAAACTGTTTGATGAGAT
TAATCCTGAAACCAAATTAATTCCTTGTGGATTACATCTTGTTCAAAGGGAATGGTTGACCCC
ATTTGACCTGTCTTACCGAAGTCGACACTTTCACCTGGACAAGTACAAGACCATTAAGGT
GCCCATGATGTACGGTGACGGCAAGTTTGCTCCACCTTTGACAAGAATTTTCGTTGTCATGT
CCTCAAACCTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCTCATGGAGAAAATGGGTGA
CCACCTCGCCCTTGAAGACTACCTGACCACAGACTTGGTGGAGACATGGCTCAGAAACATGAA
AACCAGAAACATGGAAGTTTTCTTCCGAAGTTCAAGCTAGATCAGAAGTATGAGATGCATGA
GCTGCTTAGGCAGATGGGAATCAGAAGAATCTTCTCACCTTTGCTGACCTTAGTGAACCTC
AGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTTACGAAGAACAGTGATTGAAGTTGATGA
AAGGGGCACTGAGGCAGTGGCAGGAATCTTGTCAGAAATTACTGCTATTCCATGGCTCCCTGT
CATCAAAGTGGACCGGCCATTTTCATTTATGATCTATGAAGAAACCTCTGGAATGCTTCTGTT
TCTGGGCAGGGTGGTGAATCCGACTCTCCTATAATTCAGGACATGCATAAGCACTTCGTGCTG
TAGTAGATGCTGAATCTGAGGTATCAACACACACAGGATACCAAGCAATGGATGGCAGGGGAG
AGTGTTCCTTTTGTTCTTAAGTATGTTAGGGTGTTCTCAAATAAATACAGTAGTCCCCACTTA
TCTGAGGGGGATACATTCAAAGACCCCCAGCAGATGCCGAAACGGTGGACAGTGCTGAACCT
TATATATATTTTTTCCATACATACATACCTATGATAAAGTTTAATTTATAAATTAGGCACAG
TAAGAGATTAAACATAATAACACATTAAGTAAATGAGTTACTGAACGCAAGCACTGCAAT
ACCATAACAGTCAAACCTGATTATAGAGAAGGCTACTAAGTGACTCATGGGCGAGGAGCATAGA
CAGTGTGGAGACATTGGGCAAGGGGAGAAATTCACATCCTGGGTGGGACAGAGCAGGACCATGC
AAGATTCCATCCCACTACTCAGAATGGCATGCTGCTTAAGACTTTTAGATTGTTTATTCTGG
AATTTTTCATTTAATGTTTTGGACCATGGTTGACCATGGTTAACTGAGACTGCAGAAAGCAA
AACCATGGATAAGGGAGGACTACTACAAAAGCATTAAATTGATACATATTTTTTAAAAAAA
AAAAA

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FIGURE 498

MKVVPSLLLSVLLAQVWLVPGLAPSPQSPETPAPQNQTSRVVQAPREEEDEQEASEEKAGEE
EKAWLMASRQQLAKETSNFGFSLRRKISMRRHDGNMVFSPPGMSLAMTGLMLGATGPTE'QIKR
GLHLQALKPTKPGLLPSLFKGLRETLNRNLELGLSQGSFAFIHKDFDVKETFFNLSKRYFDTE
CVPMNFRNASQAKRLMNHYINKETRGKIPKLEDEINPETKLILVDYILFKGKWLTFDPVFTE
VDTFHLDKYKTIKVPMMYGAGKFASTFDKNFRCHVLKLPYQGNATMLVVLMEKMGDHLALEDY
LTIDLIVETWLRNMKTRNMEVFFPKFKLDQKYEMHELLRQMGIRRI'FSPFADLSELSATGRNLQ
VSRVLRRTVIEVDERGTEAVAGILSEITAYSMPPVIKVDRPFHFMIYEETSGMLLFLGRVNP
TLL

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FIGURE 500

MDSLRLKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLAT
LQEAATTQENVAWRKNWMVGEGGASGRSP

Important features:

Signal peptide:

amino acids 1-18

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FIGURE 501

[illegible]

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FIGURE 502

MGPSTPLLLILFLLSWSGPLQGQHHLVEYMERRLAALAEERLAQCQDQSSRHAAELRDFKNKML
PLLEVAEKEREALRTEADTISGRVDRLEREVDYLETONPALPCVEFDEKVTGGPGTKGKGRRN
EKYDMVTDCCYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRLRDF
TLAMAARKASRVRVFPWVGTLVYGGFLYFARRPPGRPGGGEMENTLQLIKFHLANRTVV
DSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCCLAKLDPQTLDTQQWDTP
CPRENAEAAAFVICGTLYVVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAHASLRYN
PRERQLYAWDDGYQIVYKLEMRKKEEV

Important features:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 177-180, 248-251